

QY 1 MAESLPFTLETYSWSELEAWEDLOEVLSDEIGTYISSPGNEEESKFTTLDPA 60
 DB 1 MAESLPFTLETYSWSELEAWEDLOEVLSDEIGTYISSPGNEEESKFTTLDPA 60
 QY 61 AWLTPEPTEVTRTSQSPSPSSSSMAOEEDOG 97
 DB 61 AWLTPEPTEVTRTSQSPSPSSSSMAOEEDOG 97

RESULT 3

S33798
 FUS/CHOP mutant fusion protein - human
 N:Alternate names: TLS/CHOP mutant fusion protein

C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 30-Nov-1995 #text_change 30-Jun-2001
 C:Accession: S33798; S36158
 R:Crossref: A.; Aman, P.; Mandahl, N.; Ron, D.
 Nature 363, 640-644, 1993
 A>Title: Fusion of CHOP to a novel RNA-binding protein in human myxoid liposarcoma.
 A:Reference number: S33798; MUID:93288139
 A:Accession: S33798

A:Molecule type: mRNA
 A:Residues: 1-462 <CRO>
 A:Cross-references: GB:S62138; NID:9386458; PIDN:AA827103.1; PID:9386159
 R:Rabbit, T.H.; Forrester, A.; Larson, R.; Nathan, P.
 Nature Genet. 4, 175-180, 1993
 A>Title: Fusion of the dominant negative transcription regulator CHOP with a novel gene
 A:Reference number: S36157; MUID:93350637
 A:Accession: S36158
 A:Molecule type: mRNA
 A:Residues: 1-462 <RAB>
 A:Cross-references: EMBL:X71427; NID:9395919; PIDN:CA50558.1; PID:94210364
 C:Comment: This sequence is the chimeric product of a translocation mutation.
 C:Genetics:
 A:Gene: GADD153/FUS
 A:Map position: 12q13/16p11
 A:Note: TLS is a synonym for GDB:FUS
 C:Keywords: fusion protein

Query Match 84.7%; Score 430.5; DB 4; Length 462;
 Best Local Similarity 85.0%; Pred. No. 1.6e-33;
 Matches 85; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 MAESLPFTLETYSWSELEAWEDLOEVLSDEIGTYISSPGNEEESKFTTLDPA 60
 DB 294 MAESLPFTLETYSWSELEAWEDLOEVLSDEIGTYISSPGNEEESKFTTLDPA 60
 QY 61 AWLTPEPTEVTRTSQSPSPSSSSMAOEEDOG 99
 DB 354 AWLTPEPTEVTRTSQSPSPSSSSMAOEEDOG 99

RESULT 4
 JCI169
 DNA-damage-inducible protein GADD153 - human
 C:Species: Homo sapiens (man)
 C>Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 21-Jul-2000
 R:Patel, J.S.; Luehly, J.D.; Wang, M.G.; Fargnoli, J.; Fornace Jr., A.J.; McBride, O.W.;
 Gene 116, 259-267, 1992
 A>Title: Isolation, characterization and chromosomal localization of the human GADD153
 A:Reference number: JCI169; MUID:92333899
 A:Accession: JCI169
 A:Molecule type: mRNA
 A:Residues: 1-168 <PAB>
 A:Cross-references: GB:S40706; NID:9252001; PIDN:AA822646.1; PID:9252002
 C:Comment: This protein is responsible for the growth arrest.
 C:Genetics:
 A:Gene: GADD153
 C:Keywords: transcription regulation

Query Match 82.9%; Score 421; DB 2; Length 168;
 Best Local Similarity 85.0%; Pred. No. 3.5e-33;
 Matches 85; Conservative 5; Mismatches 8; Indels 2; Gaps 2;

QY 1 MAESLPFTLETYSWSELEAWEDLOEVLSDEIGTYISSPGNEEESKFTTLDPA 60
 DB 1 MAESLPFTLETYSWSELEAWEDLOEVLSDEIGTYISSPGNEEESKFTTLDPA 60
 QY 61 AWLTPEPTEVTRTSQSPSPSSSSMAOEEDOG 99
 DB 60 AWLTPEPTEVTRTSQSPSPSSSSMAOEEDOG 99

RESULT 5

JC5660
 hepatoma-derived growth factor - mouse
 N:Alternate names: HDGF

C:Species: Mus musculus (house mouse)
 C>Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 17-Mar-1999
 C:Accession: JC5660
 R:Izumoto, Y.; Kuroda, T.; Harada, H.; Kishimoto, T.; Nakamura, H.
 Biochem. Biophys. Res. Commun. 238, 26-32, 1997
 A>Title: Hepatoma-derived growth factor belongs to a gene family in mice showing sign
 A:Reference number: JC5660; MUID:97445118
 A:Accession: JC5660
 A:Molecule type: mRNA
 A:Residues: 1-237 <IGU>
 A:Cross-references: DDBJ:D63707
 C:Comment: This protein translocates to the nucleus and directly functions in mitogen
 F:115-170/Region: hatch #status predicted
 F:115-170/Region: nuclear location signal

Query Match 19.1%; Score 97; DB 2; Length 237;
 Best Local Similarity 30.9%; Pred. No. 0.053;
 Matches 30; Conservative 6; Mismatches 25; Indels 36; Gaps 3;

QY 30 SDEIGTYISSP-----GNEEESKFTTLDPA 61
 DB 132 SDEIGTYISSP-----GNEEESKFTTLDPA 61
 QY 62 WLTPEPTEVTRTSQSPSPSSSSMAOEEDOG 98
 DB 187 --GERPLPEVEKNS-TPSEPDSCGPPAEEDGEE 220

RESULT 6
 F84770
 hypothetical protein At2g35600 [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84770
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: F84770
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-263 <STO>
 A:Cross-references: GB:AE002093; NID:93608128; PIDN:AAC36161.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g35600
 A:Map position: 2

Query Match 18.5%; Score 94; DB 2; Length 263;
 Best Local Similarity 25.8%; Pred. No. 0.12;
 Matches 31; Conservative 19; Mismatches 42; Indels 28; Gaps 7;

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OM protein - protein search, using sw model

Run on: June 18, 2002, 15:08:21 ; Search time 16.39 seconds
(without alignments)

580.405 Million cell updates/sec

Title: US-09-637-550-3

Sequence: 1 MAESLPFTLETYSWELAE.....RSPDSSQSSMAQEEEEEEOG 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-71:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	100.0	168	2 S26148	nuclear protein ch
2	435	85.6	168	2 A34096	DNA damage inducib
3	430.5	84.7	462	4 S33798	FUS/CHOP mutant fu
4	421	82.9	168	2 JC1169	DNA-damage-inducib
5	97	19.1	237	2 JC5660	hepatoma-derived g
6	94	18.5	263	2 F84770	hypothetical prote
7	83.5	16.4	440	2 S49765	TYA protein - years
8	83.5	16.4	440	2 S45737	TYA protein - years
9	83.5	16.4	1755	2 S45736	TYB protein - years
10	81.5	16.0	214	2 T39559	probable ubiquinol
11	81.5	16.0	1624	2 T25592	hypothetical prote
12	81	15.9	297	2 S76306	hypothetical prote
13	80.5	15.8	303	2 A86443	probable major int
14	80.5	15.8	440	2 S69970	TYA protein - years
15	80.5	15.8	1034	2 D96519	myosin-like protei
16	80.5	15.8	1755	2 S69969	TYB protein - years
17	80.5	15.7	240	2 A55055	hepatoma-derived g
18	78.5	15.5	440	2 S52895	TYA protein - years
19	77.5	15.3	872	2 T25186	hypothetical prote
20	77.5	15.3	1840	2 T30250	CTL protein - mous
21	76	15.0	296	2 A54527	110k antigen - pla
22	75.5	14.9	3375	2 T19821	hypothetical prote
23	75	14.8	310	2 T46987	bone sialoprotein
24	74	14.6	344	2 T40167	hypothetical prote
25	74	14.6	418	2 T15827	hypothetical prote
26	73.5	14.5	187	2 B86704	hypothetical prote
27	73.5	14.5	382	2 J01122	gas-vesicle protei
28	73.5	14.5	382	2 T08243	gas-vesicle operon
29	73.5	14.5	550	2 T29919	hypothetical prote

30	73.5	14.5	1114	2 T50222	deltaE1 - chicken
31	73	14.4	113	2 C89828	conserved hypothet
32	73	14.4	648	2 H84587	probable WD-40 rep
33	72.5	14.3	349	2 T42965	glycoprotein - ate
34	72	14.2	617	2 A56051	myocyte nuclear fa
35	72	14.2	1171	2 T13065	p182 protein - fr
36	72	14.2	2232	2 T34434	hypothetical prote
37	71.5	14.1	449	2 A41520	chromogranin A pre
38	71.5	14.1	1210	2 T39410	AF-4 protein, spli
39	71.5	14.1	1213	2 A58198	serine/proline-ric
40	71	14.0	309	2 T00503	probable MYB famil
41	71	14.0	757	2 S68142	probable transcrip
42	71	14.0	1117	2 JC4934	delta-crystallin/
43	70.5	13.9	185	2 C70550	hypothetical prote
44	70.5	13.9	555	2 A56560	zinc finger protei
45	70.5	13.9	672	2 T12524	hypothetical prote

ALIGNMENTS

RESULT 1
S26148
nuclear protein chop-10 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S26148
R:Ron. D.; Habener, J.F.
Genes Dev. 6, 439-453, 1992
A>Title: CHOP, a novel developmentally regulated nuclear protein that dimerizes with
A:Reference number: S26148; MUID:92192456
A:Accession: S26148
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-168 <ROR>
A:Cross-references: EMBL:X67083; NID:q50406; PIDN:CAA47465.1; PID:q50407
C:Keywords: transcription regulation

Query Match 100.0%; Score 508; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.7e-41;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAESLPFTLETYSWELAEWDLEVLSSDIEGTYISFGNEEESKFTTIDPSSL 60
DB 1 MAESLPFTLETYSWELAEWDLEVLSSDIEGTYISFGNEEESKFTTIDPSSL 60
OY 61 AWLTERPGTEVTRTSQSPRSPDSSQSSMAQEEEEEEOG 99
DB 61 AWLTERPGTEVTRTSQSPRSPDSSQSSMAQEEEEEEOG 99
RESULT 2
A34096
DNA damage inducible protein - Chinese hamster
C:Species: Citicellus griseus (Chinese hamster)
C:Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A34096
R:Porcine Jir., A.J.; Nebert, D.W.; Hollander, M.C.; Luetthy, J.D.; Papathanasiou, M.;
Mol. Cell. Biol. 9, 4196-4203, 1989
A>Title: Mammalian genes coordinately regulated by growth arrest signals and DNA-dama
A:Reference number: A34096; MUID:9006424
A:Accession: A34096
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-168 <ROR>
A:Cross-references: GB:M29238; NID:q191077; PIDN:AAA36982.1; PID:q304507
C:Keywords: transcription regulation

Query Match 85.6%; Score 435; DB 2; Length 168;
Best Local Similarity 88.7%; Pred. No. 1.6e-34;
Matches 86; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: June 18, 2002, 15:09:51 ; Search time 11.83 seconds

(without alignments)
324.027 Million cell updates/sec

Title: US-09-637-550-3

Perfect score: 508
Sequence: 1 MAESLPFTLETIVSWLEA.....RSPDSSQSSMAQEEEEEEOG 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	168	1	GA15_MOUSE
2	435	85.6	168	1	GA15_MOUSE
3	430.5	84.7	169	1	GA15_HUMAN
4	88	17.3	237	1	HDFG_MOUSE
5	80	15.7	240	1	HDFG_MOUSE
6	78.5	15.5	440	1	YMT6_YEAST
7	76	15.0	296	1	110K_PLAKN
8	75	14.8	310	1	SIAL_BOVIN
9	74	14.6	418	1	YSE2_CAEEL
10	74	14.6	701	1	CGI_HUMAN
11	73.5	14.5	187	1	RPOE_LACTA
12	73.5	14.5	382	1	GCCL_HALNT
13	73.5	14.5	1114	1	TCF8_CHICK
14	73.5	14.5	3726	1	ABF1_MOUSE
15	72.5	14.3	1548	1	SMCY_MOUSE
16	72	14.2	617	1	FXK1_MOUSE
17	71.5	14.1	394	1	MYC1_CYPCA
18	71.5	14.1	506	1	TUB_HUMAN
19	71.5	14.1	1210	1	AP4_HUMAN
20	71	14.0	1110	1	Y556_HUMAN
21	71	14.0	1117	1	TCF8_MOUSE
22	71	14.0	1878	1	BRC1_CANFA
23	70.5	13.9	393	1	P53_MACPA
24	70.5	13.9	393	1	P53_MACMU
25	70.5	13.9	555	1	ZF38_MOUSE
26	70	13.8	287	1	RRP_MOUSE
27	70	13.8	297	1	RRP_MOUSE
28	70	13.8	406	1	MYC_MOUSE
29	70	13.8	414	1	NSR1_YEAST
30	70	13.8	500	1	GAR2_SCHPO
31	69.5	13.7	449	1	CMCA_BOVIN
32	69.5	13.7	732	1	NPH1_HUMAN
33	69.5	13.7	966	1	SSNE_YEAST

ALIGNMENTS

34	69.5	13.7	1574	1	SV11_RAT	062910	rattus norv
35	69.5	13.7	1647	1	SN24_HUMAN	P51532	homo sapien
36	69.5	13.7	1805	1	NEST_RAT	P21263	rattus norv
37	69.5	13.6	1080	1	SET1_YEAST	P05432	rattus norv
38	68.5	13.5	459	1	ZF38_HUMAN	P05432	rattus norv
39	68.5	13.5	473	1	RGPI_HUMAN	P07298	homo sapien
40	68.5	13.5	587	1	VNCS_PAVHB	P07298	homo sapien
41	68.5	13.5	671	1	OKRP_RAT	P07298	homo sapien
42	68.5	13.5	999	1	PTPG_CHICK	P06361	rattus norv
43	68.5	13.5	1422	1	VIT_CHICK	P06361	rattus norv
44	68.5	13.5	1823	1	VIT_CHICK	P06361	rattus norv
45	68	13.4	393	1	P53_CERAE	P13481	cercopithec

RESULT 1
GA15_MOUSE STANDARD: PRT: 168 AA.
AC P35639;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Growth arrest and DNA-damage-inducible protein GADD153 (DNA-damage
inducible transcript 3) (DDIT3) (C/EBP-homologous protein) (CHOP).
GN DDIT3 OR CHOP OR GADD153.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC SPRAIN-SWISS:
RX MEDLINE=92192456; PubMed=1547942;
RA Ron D., Habener J.F.;
RT "CHOP, a novel developmentally regulated nuclear protein that
dimerizes with transcription factors C/EBP and LAP and functions as a
RT dominant-negative inhibitor of gene transcription.";
RL Genes Dev. 6:439-453(1992).
CC - FUNCTION: INHIBITS THE DNA-BINDING ACTIVITY OF C/EBP AND LAP BY
CC - FORMING HETERODIMERS THAT CANNOT BIND DNA.
CC - SUBUNIT: HETERODIMER.
CC - SUBCELLULAR LOCATION: Nuclear.
CC - SIMILARITY: SOME, TO BZIP PROTEINS.
CC - This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: X67083; CAA47465.1;
CC PIR: S26148; S26148.
CC TRANSFAC: T00127;
CC MGD: MGI:109247; Ddit3.
CC InterPro: IPR001871; bzip.
CC SMART: SM00338; BRLZ.1.
CC Growth arrest, Nuclear protein; Transcription regulation; Repressor.
FT DOMAIN 92 97
FT POLY-GLO.
FT LEUCINE-ZIPPER.
SQ SEQUENCE 168 AA; 19189 MW; CAA23B79512F33AB CRC64;
Query Match 100.0%; Score 508; DB 1; Length 168;
Best local similarity 100.0%; Pred. No. 1.4e-41;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MAESLPFTLETIVSWLEAWEDLOEVLSDDIGGIYSSPGNEESKFTTLDPAFL 60
1 MAESLPFTLETIVSWLEAWEDLOEVLSDDIGGIYSSPGNEESKFTTLDPAFL 60

QY 61 AMLEPPEPTVTRTSOSPRSPSSSSMAOEEREEEG 99
 DB 61 AMLEPPEPTVTRTSOSPRSPSSSSMAOEEREEEG 99

RESULT 2
 ID GA15_CRITLO STANDARD; PRT; 168 AA.
 AC P14607;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Growth arrest and DNA-damage-inducible protein GADD153 (DNA-damage
 DE Inducible transcript 3) (DDIT3) (C/EBP-homologous protein) (CHOP).
 GN DDIT3 OR CHOP OR GADD153.
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Cricetus.
 CC NCBI_TaxID=10030;
 CC [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=90066424; PubMed=2573827;
 RA Fornace A.J. Jr., Nebert D.W., Holbrook N.J., Luetthy J.D.,
 RA Papathanasiou M., Fargnoli J., Holbrook N.J.,
 RT "Mammalian genes coordinately regulated by growth arrest signals and
 RT DNA-damaging agents.";
 RL Mol. Cell. Biol. 9:4196-4203(1989).
 CC -1 FUNCTION: INHIBITS THE DNA-BINDING ACTIVITY OF C/EBP AND LAP BY
 CC FORMING HETERODIMERS THAT CANNOT BIND DNA.
 CC -1 FUNCTION: MAY PLAY A ROLE IN THE INHIBITION OF GROWTH AFTER
 CC DNA DAMAGE AS WELL AS IN THE MAINTENANCE OF GROWTH ARREST IN G0.
 CC -1 SUBUNIT: HETERODIMER.
 CC -1 SUBCELLULAR LOCATION: Nuclear.
 CC -1 SIMILARITY: SOME, TO BZIP PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M29238; AAA36982.1;
 DR PIR: A34096; A34096.
 DR TRANSFAC: T00299;
 DR InterPro: IPR001871; bZIP.
 DR SMART: SM00338; BRLZ, 1.
 KW Growth arrest; Nuclear protein; Transcription regulation; Repressor.
 FT DOMAIN 92 95 POLY-GLU.
 FT LEUCINE-ZIPPER.
 FT 133 147
 FT 168 AA; 18831 MW; 5FD5A2A6C5228771 CRC64;
 SQ SEQUENCE

Query Match 85.6%; Score 435; DB 1; Length 168;
 Best Local Similarity 88.7%; Pred. No. 1.2e-34;
 Matches 86; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAESLPFTLETVSSWELAWYEDLOEVLSDGIGTYISSPGNEEESKFTTIDPASTL 60
 DB 1 MAESLPFTLETVSSWELAWYEDLOEVLSDGIGTYISSPGNEEESKFTTIDPASTL 60

QY 61 AMLEPPEPTVTRTSOSPRSPSSSSMAOEEREEEG 97
 DB 61 AMLEPPEPTVTRTSOSPRSPSSSSMAOEEREEEG 97

RESULT 3
 ID GA15_HUMAN STANDARD; PRT; 169 AA.
 AC P35638;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth arrest and DNA-damage-inducible protein GADD153 (DNA-damage
 DE Inducible transcript 3) (DDIT3) (C/EBP-homologous protein) (CHOP).
 GN DDIT3 OR CHOP OR GADD153.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=92339899; PubMed=1339368;
 RX Park J.S., Luetthy J.D., Wang M.G., Fargnoli J., Fornace A.J. Jr.,
 RA McBride O.W., Holbrook N.J.,
 RT "Isolation, characterization and chromosomal localization of the
 RT human GADD153 gene.";
 RL Gene 116:259-267(1992).
 CC [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=93288139; PubMed=8510758;
 RA Crozat A., Aman P., Mandahl N., Ron D.,
 RT "Fusion of CHOP to a novel RNA-binding protein in human myxoid
 RT liposarcoma.";
 RL Nature 363:640-644(1993).
 CC [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=93350637; PubMed=7503811;
 RA Raddilts T.H., Forster A., Larson R., Nathan P.,
 RT "Fusion of the dominant negative transcription regulator CHOP with a
 RT novel gene FUS by translocation t(12;16) in malignant liposarcoma.";
 RL Nat. Genet. 4:175-180(1993).
 CC -1 FUNCTION: INHIBITS THE DNA-BINDING ACTIVITY OF C/EBP AND LAP BY
 CC FORMING HETERODIMERS THAT CANNOT BIND DNA.
 CC -1 SUBUNIT: HETERODIMER.
 CC -1 SUBCELLULAR LOCATION: Nuclear.
 CC -1 DISEASE: A FORM OF MIXOID LIPOSARCOMA IS CHARACTERIZED BY A
 CC CHROMOSOMAL TRANSLOCATION T(12;16)(Q13;P11) THAT INVOLVES DDIT3
 CC AND FUS.
 CC -1 SIMILARITY: SOME, TO BZIP PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S40706; AAB22646.1;
 DR PIR: S62138; AAB27103.1; ALT_INIT.
 DR PIR: JC1169; JC1169.
 DR TRANSFAC: T01387;
 DR MIM: 126337;
 DR MIM: 151900;
 DR InterPro: IPR001871; bZIP.
 DR SMART: SM00338; BRLZ, 1.
 KW Growth arrest; Nuclear protein; Transcription regulation; Repressor;
 KW Chromosomal translocation; Proto-oncogene.
 FT DOMAIN 93 97 POLY-GLU.
 FT LEUCINE-ZIPPER.
 FT 134 148
 FT 169 AA; 19175 MW; 319052934FBIFFB2 CRC64;
 SQ SEQUENCE

Query Match 84.7%; Score 430.5; DB 1; Length 169;
 Best Local Similarity 85.0%; Pred. No. 3.3e-34;
 Matches 85; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 MAESLPFTLETVSSWELAWYEDLOEVLSDGIGTYISSPGNEEESKFTTIDPASTL 60
 DB 1 MAESLPFTLETVSSWELAWYEDLOEVLSDGIGTYISSPGNEEESKFTTIDPASTL 60

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 15:08:56 ; Search time 24.64 Seconds
(without alignments)
695,069 Million cell updates/sec

Title: US-09-637-550-3

Perfect score: 508
Sequence: 1 MAESLPFTLETYSWLEA.....RSPDSSQSSMAOEEREEG 99

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	98.6	168	11 Q91YW9	Q91YW9 mus musculus
2	485	95.5	168	11 Q62804	Q62804 rattus norv
3	485	95.5	168	11 Q62857	Q62857 rattus norv
4	97	19.1	237	11 Q9CYA4	Q9CYA4 mus musculus
5	97	19.1	237	11 Q9JX87	Q9JX87 mus musculus
6	94	18.5	263	10 Q82281	Q82281 arabidopsis
7	91.5	18.0	674	2 Q9F865	Q9F865 enterococcu
8	90.5	17.8	627	2 Q9F864	Q9F864 enterococcu
9	90.5	17.8	627	2 Q9F863	Q9F863 enterococcu
10	89	17.5	237	11 Q923W3	Q923W3 rattus norv
11	87.5	17.2	458	2 Q9XBQ7	Q9XBQ7 enterococcu
12	87.5	17.2	580	2 Q9F861	Q9F861 enterococcu
13	87.5	17.2	721	2 Q9F866	Q9F866 enterococcu
14	85.5	16.8	721	2 Q9F867	Q9F867 enterococcu
15	83.5	16.4	440	3 Q03964	Q03964 saccharomyc
16	83.5	16.4	440	3 Q12266	Q12266 saccharomyc

17	83.5	16.4	1755	3 Q12490	Q12490 saccharomyc
18	83	16.3	331	4 Q9H7H3	Q9H7H3 homo sapien
19	82.5	16.2	580	2 Q9F862	Q9F862 enterococcu
20	81.5	16.0	214	3 Q42932	Q42932 schizosacch
21	81.5	16.0	675	11 Q91YW9	Q91YW9 mus musculus
22	81.5	16.0	1123	11 Q9BDD5	Q9BDD5 mus musculus
23	81.5	16.0	1138	5 Q95077	Q95077 caenorhabd1
24	81.5	16.0	1636	5 Q95078	Q95078 caenorhabd1
25	81	15.9	248	10 Q9LRH2	Q9LRH2 raphanus sa
26	81	15.9	297	16 P74789	P74789 synchocyst
27	80.5	15.8	303	10 Q9C6S9	Q9C6S9 arabidopsis
28	80.5	15.8	440	3 Q12391	Q12391 saccharomyc
29	80.5	15.8	1054	10 Q9C698	Q9C698 arabidopsis
30	80.5	15.8	1755	3 Q12112	Q12112 saccharomyc
31	79	15.6	1460	5 Q9G779	Q9G779 leishmania
32	78.5	15.5	271	5 Q9V8B2	Q9V8B2 drosophila
33	78.5	15.5	931	4 Q9HCH8	Q9HCH8 homo sapien
34	77.5	15.3	872	5 Q9XU67	Q9XU67 caenorhabd1
35	77.5	15.3	1840	11 Q61818	Q61818 mus musculus
36	77	15.2	250	11 Q9JMG6	Q9JMG6 rattus norv
37	77	15.2	516	2 Q9ERT5	Q9ERT5 corynebacte
38	77	15.2	721	13 Q9DGL1	Q9DGL1 fuqu rubrip
39	77	15.2	1030	5 Q9G2B3	Q9G2B3 helioverpa
40	76	15.0	479	4 Q9NQ22	Q9NQ22 homo sapien
41	76	15.0	896	4 Q9COE4	Q9COE4 homo sapien
42	75.5	14.9	323	6 Q951V7	Q951V7 macaca fasc
43	75.5	14.9	413	4 Q15417	Q15417 homo sapien
44	75.5	14.9	925	5 Q9UT88	Q9UT88 caenorhabd1
45	75.5	14.9	3375	5 Q9XRT5	Q9XRT5 caenorhabd1

ALIGNMENTS

RESULT 1
Q91YW9 ID Q91YW9 PRELIMINARY: PRT; 168 AA.
AC Q91YW9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DNA-DAMAGE INDUCIBLE TRANSCRIPT 3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013718; AAH13718.1; -
SQ SEQUENCE 168 AA; 19190 MW; CC993B7957F43160 CRC64;

Query Match 98.6%; Score 501; DB 11; Length 168;
Best Local Similarity 99.0%; Pred. No. 3.1e-44;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAESLPFTLETYSWLEAWEDLOEVLSDEIGTYSFGNEEESKTTTIDPASTL 60
DB 1 MAESLPFTLETYSWLEAWEDLOEVLSDEIGTYSFGNEEESKTTTIDPASTL 60
QY 61 AWLIEPPTLETYSWLEAWEDLOEVLSDEIGTYSFGNEEESKTTTIDPASTL 60
DB 61 AWLIEPPTLETYSWLEAWEDLOEVLSDEIGTYSFGNEEESKTTTIDPASTL 60

RESULT 2
Q62804 ID Q62804 PRELIMINARY: PRT; 168 AA.
AC Q62804;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

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DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE GADD153.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen C.H., Nussenzweig A., Li G., Ling C.C.;
RT "Cloning of rat GADD153 and its expression in rat cells.";
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nussenzweig A.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U30186; AAA73629.1; -.
DR InterPro; IPR001871; bZIP.
DR SMART; SM00338; BRLZ; 1.
SQ
SEQUENCE 168 AA; 18996 MW; 2516D983D40EA6E1 CRC64;

Query Match          95.5%; Score 485; DB 11; Length 168;
Best Local Similarity 94.9%; Pred. No. 1.4e-42;
Matches 94; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MAESLPFTLETVSSWELAWYEDLOEVLSSDEIGTYISSPGNEESKFTTLDPASL 60
DB 1 MAESLPFAFETVSSWELAWYEDLOEVLSSDEIGTYISSPGNEESKFTTLDPASL 60
OY 61 AMLEPPTVETRTSQRSPDSSQSSMAOEEDDGG 99
DB 61 AMLEPPTVETRTSQRSPDSSQSSMAOEEDDGG 99

RESULT 3
ID 062857 PRELIMINARY; PRT; 168 AA.
AC 062857;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE GADD153.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE DAWLEY; TISSUE-BRAIN;
RA Jin K.L., Chen J., Simon R.P., Graham S.H.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U36994; AAA87944.1; -.
DR InterPro; IPR001871; bZIP.
DR SMART; SM00338; BRLZ; 1.
SQ
SEQUENCE 168 AA; 19013 MW; 251716CD712BA6E1 CRC64;

Query Match          95.5%; Score 485; DB 11; Length 168;
Best Local Similarity 94.9%; Pred. No. 1.4e-42;
Matches 94; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MAESLPFTLETVSSWELAWYEDLOEVLSSDEIGTYISSPGNEESKFTTLDPASL 60
DB 1 MAESLPFAFETVSSWELAWYEDLOEVLSSDEIGTYISSPGNEESKFTTLDPASL 60
OY 61 AMLEPPTVETRTSQRSPDSSQSSMAOEEDDGG 99
DB 61 AMLEPPTVETRTSQRSPDSSQSSMAOEEDDGG 99

RESULT 4
ID 09CYA4 PRELIMINARY; PRT; 237 AA.
OY 09CYA4

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AC 09CYA4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HEPATOMA-DERIVED GROWTH FACTOR.
GN HDGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6J; TISSUE-EMBRIO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017863; BAB30979.1; -.
DR MGD; MGI:1194494; Hdgf.
DR InterPro; IPR000313; PWMP.
DR Pfam; PF00855; PWMP.
DR SMART; SM00293; PWMP; 1.
DR SMART; SM00293; PWMP; 1.
SQ
SEQUENCE 237 AA; 26313 MW; 0AE1CF57AD1A733C CRC64;

Query Match          19.1%; Score 97; DB 11; Length 237;
Best Local Similarity 30.9%; Pred. No. 0.03; 25; Indels 36; Gaps 3;
Matches 30; Conservative 6; Mismatches 25; Indels 36; Gaps 3;

OY 30 SSDEIGTYISSP-----GNEESKFTTLDPASIA 61
DB 132 SSDEGLIVDEPAKKNKNGTLKRRAGVLEDSPPKRGSGHDEEDKRIALE----- 186
OY 62 WLTEPPTVETRTSQRSPDSSQSSMAOEEDDGG 98
DB 187 --GERPLPVEVEKNS--TPSPDSCGCPAPAEDEEGER 220

RESULT 5
ID 09JK87 PRELIMINARY; PRT; 237 AA.
AC 09JK87;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TDRM1.
GN TDRM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C; TISSUE=THYMUS;
RA Zhao Y., Chen W., Wang Y.;
RT "Cloning of novel gene related to thymus development.";

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